

EXHIBIT 3

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

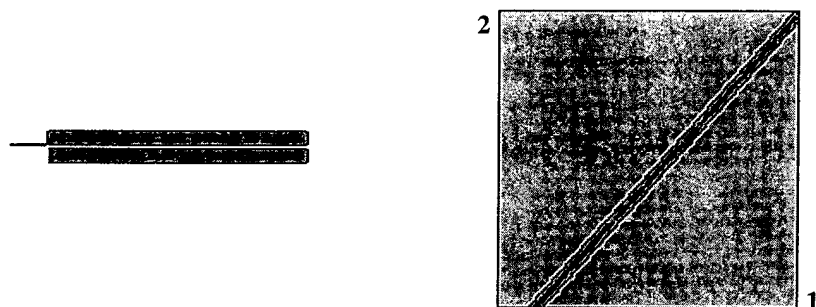
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☐ View option **Standard**
 Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: gi|1469860|dbj|BAA09787.1|leptin [Homo sapiens] >gi|4557715|ref|NP_000221.1| leptin precursor [Homo sapiens] >gi|730218|sp|P41159|LEP_HUMAN Leptin precursor (Obesity factor) (Obese protein)
 >gi|623332|gb|AAA60470.1| ob >gi|1226244|gb|AAC50400.1| obese protein >gi|1407583|dbj|BAA09839.1| ob protein
 [Homo sapiens] >gi|38174530|gb|AAH60830.1| Leptin (obesity homolog, mouse) [Homo sapiens]
 >gi|46854318|gb|AAH69527.1| Leptin (obesity homolog, mouse) [Homo sapiens] >gi|46854679|gb|AAH69452.1| Leptin
 (obesity homolog, mouse) [Homo sapiens]...
 Length = 167 (1 .. 167)

Sequence 2: gi|1813869|gb|AAB41786.1|leptin precursor [Ovis aries] >gi|3041703|sp|Q28603|LEP_SHEEP Leptin (Obesity factor)
 Length = 146 (1 .. 146)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 244 bits (624), Expect = 1e-63
 Identities = 127/146 (86%), Positives = 136/146 (93%), Gaps = 0/146 (0%)

Query	22	VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV	81
		VPI+KVQDDTKTLIKTIVTRINDISHTQSVSSKQ+VTGLDFIPGLHP+L+LSKMDQTLA+	
Sbjct	1	VPIRKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPLLKMDQTLAI	60
Query	82	YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETDSLGGVLEASGYS	141
		YQQIL S+PSRNVIQISNDLENLRDLLH+LA SKSC LP LE+L+SLG VLEAS YS	
Sbjct	61	YQQILASLPSRNVIQISNDLENLRDLLHLLAASKSCPLQVRALESLESLGVVLEASLYS	120
Query	142	TEVVALSRLQGSLQDMLWQLDLSPGC	167
		TEVVALSRLQGSLQDML QLDLSPGC	
Sbjct	121	TEVVALSRLQGSLQDMLRQLDLSPGC	146

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda	K	H
0.321	0.135	0.415

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 241

Number of extensions: 83

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 167

Length of database: 1,565,033,500

Length adjustment: 124

Effective length of query: 43

Effective length of database: 1,565,033,376

Effective search space: 67296435168

Effective search space used: 67296435168

Neighboring words threshold: 9

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.9 bits)

S2: 73 (32.7 bits)